

Template

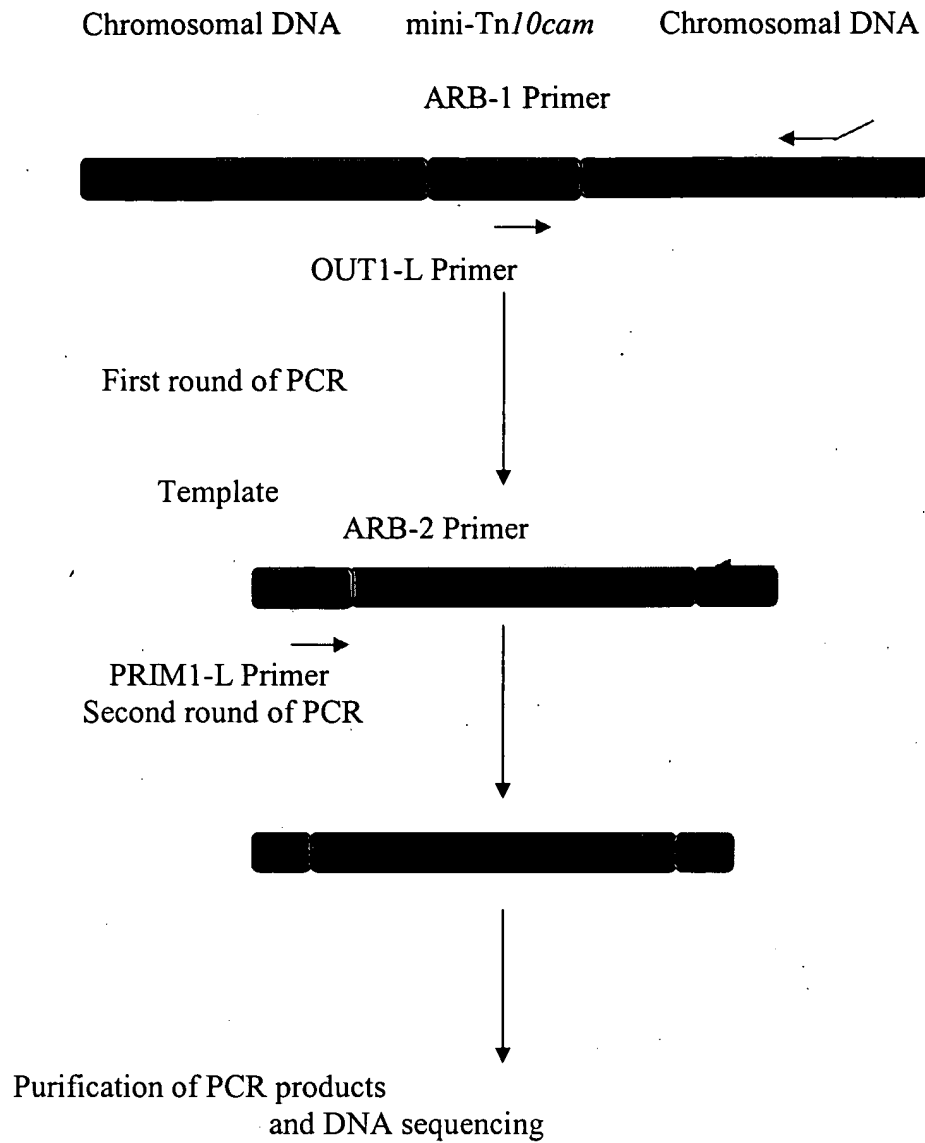
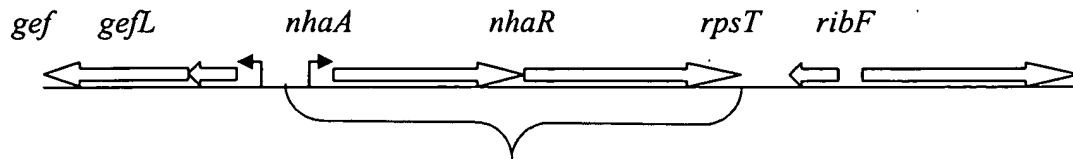
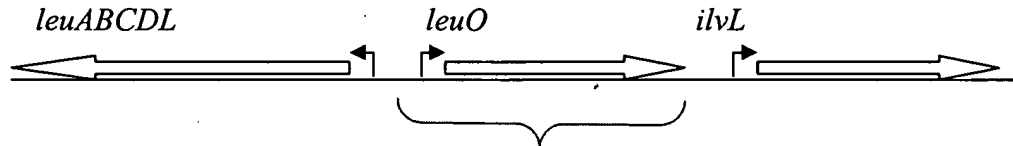


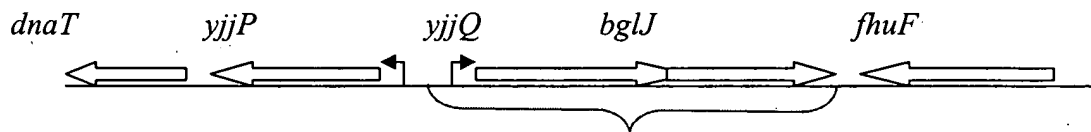
Fig. 1. Schematic diagram of Arbitrarily primed Polymerase Chain Reaction



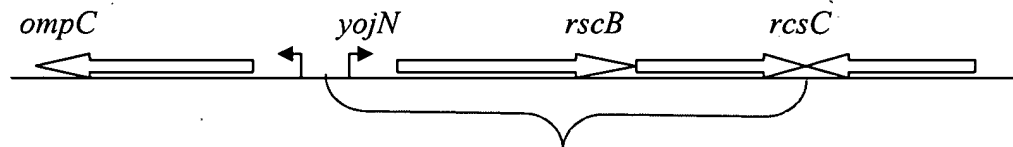
Genome included in cloning *nhaR*



Genome included in cloning *leuO*



Genome included in cloning *yjjQ*



Genome included in cloning *yojN*

Fig. 2. Genes or operons for complementation studies. Open reading frames or coding regions (\rightarrow); predicted promoters (\curvearrowright); cloned regions ($\underbrace{\hspace{1cm}}$)

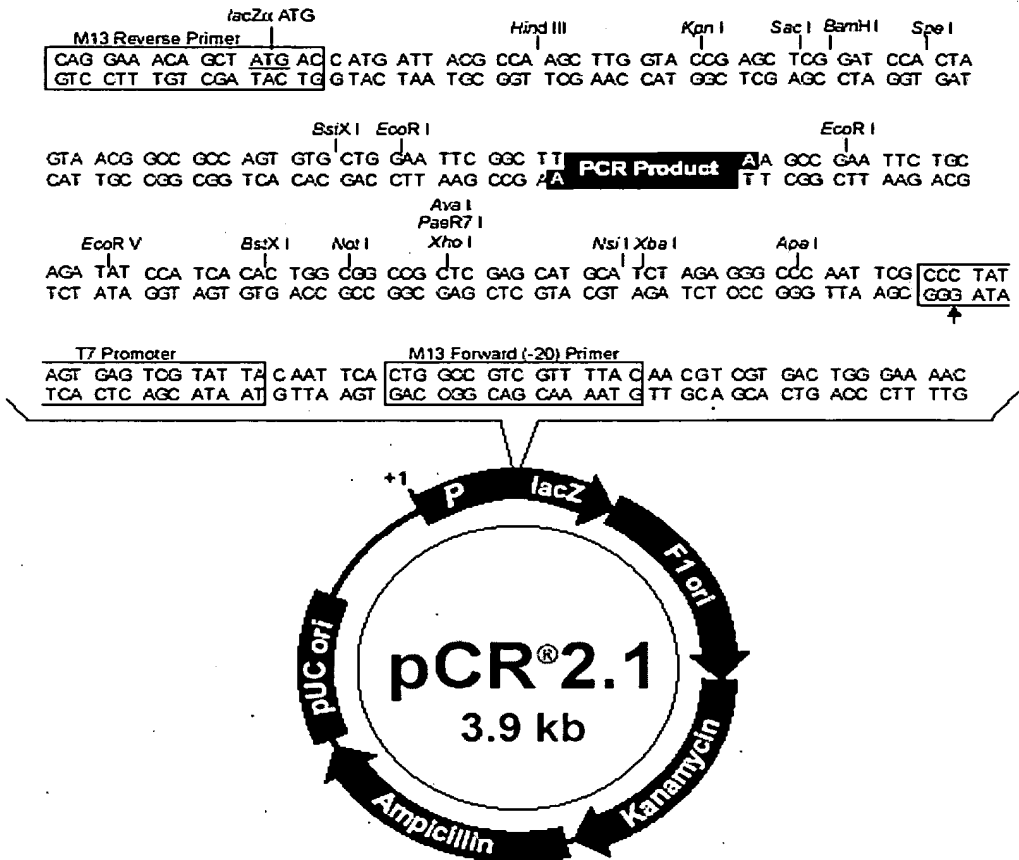


Fig. 3. Vector pCR2.1 with insertion cloning site and resistance gene for Ampicillin (Invitrogen, Carlsbad, CA)

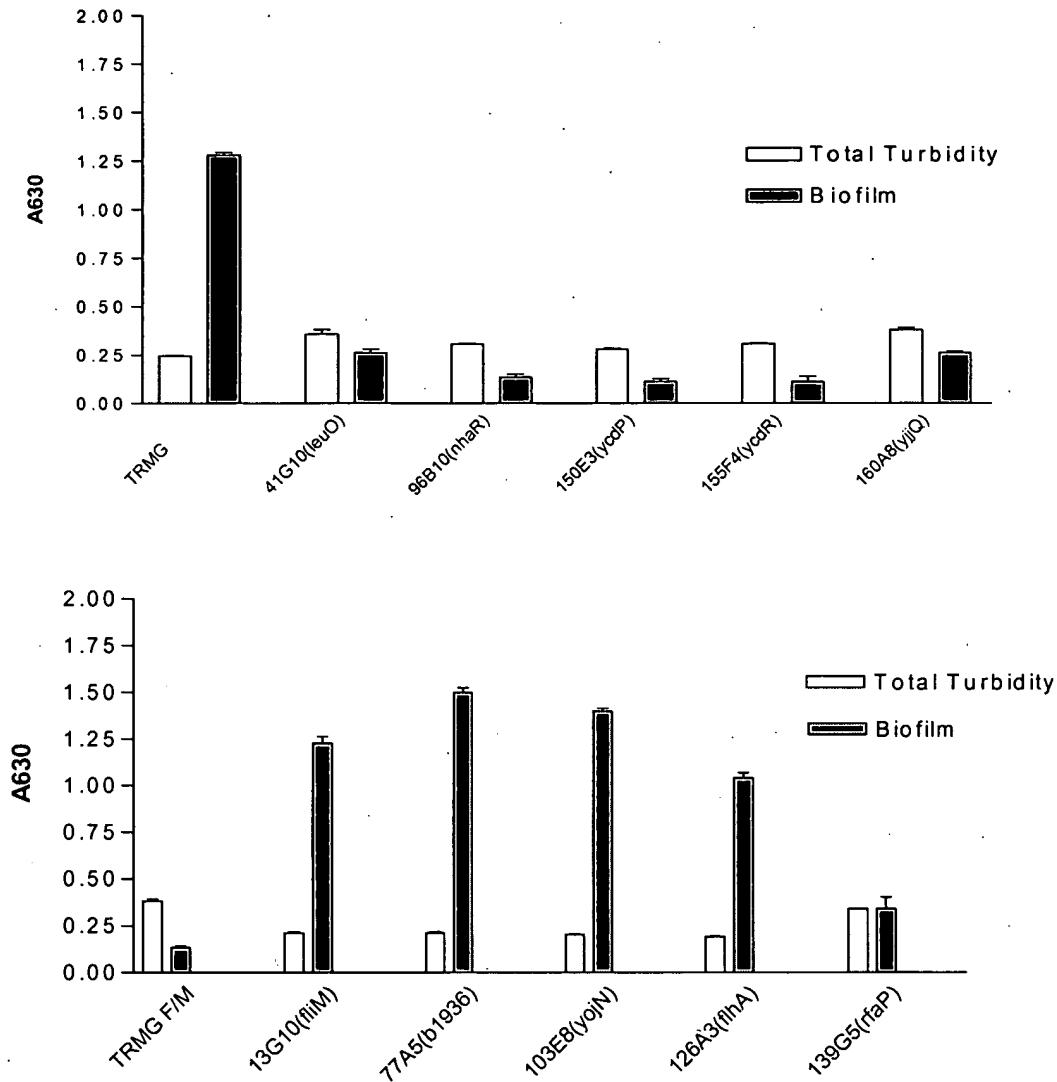


Fig. 4. Cell Growth (total turbidity at A630 before staining) and biofilm formation A630 after crystal violet staining) absorbance readings for parent strains and representative mutant strains.

- A) TRMG parent strain and biofilm-down mutants 41G10, 96B10, 150E3, 155F4 and 160A8 TRMG F/M parent strain and biofilm-up mutants 13G10, 77A5, 103E8, 126A3, and 139G5 (Upper Figure)
- B) TRMG F/M parent strain and biofilm-up mutants 13G10, 77A5, 103E8, 126A3, and 139G5 (Lower Figure)

Fig. 5

Sequences of Up Mutants

1B10 (10X)

fliD gene - flagella biosynthesis; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

AAAAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTC
ATCAG

GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAAGCGA
CGCTAACCCCCATTTCAAATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCCTACG
GTACGCTGAAAAGCGCGCTGACGACTTTCCAGACCGCCAATACTGCATTGTCTAAAG
CCGATCTTTTTTCCGCCACCAGCACCACCAGCAGCACCACCGCGTTC

12E12-6 (7x)

rfaG gene - enzyme, macromolecule metabolism; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

AAAAACGGTTACCGGATCCGG

GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG

AGTTAAGTCCCATACCAACCATGGACGCAATGCAGAATATTATGCCTGGGTACAAAATCATCTCAAAG

AGCATCCCGCAGATCGCGTTGTTGGGTTTAATAAGATGCCTGGCCTGGATGTTTATTTTGCCGCTGATG

TTTGTTACGCCGAGAAAGTTGCGCAAGAAAAAGGTTTTTTATATCGTTTAACATCACGATATCCNCNN

NNNNNGTACTAGTCGACGCGGGGCCAANN

13G10-4 (11X)

fliM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NAAAAACCCGCCGGACATCCCGGATCCGG

GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG

TGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNNCNCNCNGNACTAGTCGACGCGTGGCCA

14C10-4 (10X)

flgE gene - structural component; surface structures/ flagellar biosynthesis, hook protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74160

AACGGNCCGATCCGG

GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG

AGATCANCTGAATTCCAGTGATCCGCTTCTACTGTTACGCCATTCAANNGCCNGCAATGCGGNTANCTNTNAC

AAANAAGGTTNNGTGACTGTTTTCCACAGTCATGGTAATGCTCATGACATGAGCGTCTACTTTGTGNACCCGGG

GATAATAACTGGCAGGTCTACACCCAGGATAGCAGTGATCCAAACAGCATTGCGAAGACAGCG

36E2-5 (3X)

yhjH gene (complement) - orf; unknown function ; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_004431

Protein Accession # NP_417982

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCTTACACCTGGCAGCCGATCTATCAAACATGCGGGCGGTTAATGGCCGTGGAGCTATTAACGGTGG
TCACGCATCCCTTGAACCCCTTCGCAACGCCTGCCGCCGGATCGCTATTTACTGAAATCACCGTCAGCC
ATCGGATGGAGGTTGTGAAAGAGCAGATTGATTTGCTGGCGCAAAAAGCCGACTTCTTTATAGAGCAC
GGCCTGCTGGCATCGGTCAATAT

38G7-2 (11X)

fliM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTTCGGTATGGGTAAACTCGCGACCTTCCA
CTTTGGTTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAG
AACACCACCAGCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTTCAGGTTGGTCGGCACCGGCAG
GTTGCGGGCAAATTCATGGTACGGCTGAATGCGGATGGCCCCGACGGTTATATCCNGNCNNNNNGTAC
TAGTCGACG

39C9-2 (3X)

rep gene - enzyme; DNA replication, repair restriction/modification; product - rep helicase, a single-stranded DNA dependent ATPase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000454

Protein Accession # AAC76783

AAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCAT
CAG
TATCCAGCCCCAACGTATGGAAAGTGGAGATCATCAGCCACGCGCCTCTTTGCGCCCCAGCGTCTGC
CCTACACGCTCTTTCATCTCGCGCGCTGCTTTATTAGTAAAGGTCACCGCCGCAATGTGCCGCGCCTGA
TAACCGCAACCGCGGATCAGATGGGCGATTTTATTGGTGATAACACGAGTTTACCGGAACCCGCGCC
CGCCAGCACCAGGCAGGGGCCGTAACGAATTCGACAGCTTGTTGTTGGCCGGGGTTTAGACGCATAG
GTGTATTGCTCA

42G6-4 (12X)

fliP gene - putative structure; surface structures/ flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG

TGGTACGCATCTACATAAATTTTGTCTGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAG
CCCCAGCAATACCTGGTTAGGTGGCGCGCGGAGGGTGTTCACGCAATAAACCAAAAAAC
AATGATGATGCGGGTGAACCTGGTCATCATCAGTAAAATTGCCGGAATAAACGTCAACGAGGTGATG
AACACCAGCGTCTGCACCGGGAGC

43B10-3 (11X)

fliG gene – Structural component; surface structure, flagella motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

NNCNNAACANACGGNNCCGGCCNG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGGCGAGCTGGCGCAGAAAATCATCGACGAGATGTTCTGTTCGAGAATCTGGTGGAATNTCGCCAATCGCNGT
ACTAGTCGACGNGTGGCCAAANTGGATTCNAATCGCTGNTGATCGCGCTGAAAGGAGCCGAGCNGTCACTGT
GCNAGAANTTCTTGNCNATATGTGCNCCGTCGCCCNATATCCCNCCNACCGTACCCCTNGNACGNNNN
ACCNGNACCCCNNTNCGGNCAAGNATGNANANNANCCNGATANANCAAGNANCANTNCTNNGATNCACNNNATAN
NANNGNCGCCNAC

43F5-2 (2.5X)

wecB gene - enzyme; Central intermediary metabolism; sugar-nucleotide synthesis, product - UDP -N-
acetyl glucosamine-2-epimerase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000455

Protein Accession # AAC76791

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGCATGCTCTCGCATTCTGGAAGCGTTAAAAAATAATCGGATATCACTATGAGTTTTGCGACC
ATTTCTGTTATCGGACTGGGTTATATCGGGCTGCCAACNGCTACNCGACNCGCGCCNCGGCAAAAACA
GGTAATTGGTGTGATATCAACCAACATGCGGTTGATACCATCAATCGTGGCCAAATCCATATCCCCC
CCCCCGTACTAGTCGACG

45C8-4 (4X)

frdA gene – enzyme; energy metabolism, carbon: anaerobic respiration; product is fumarate reductase, anaerobic
flavoprotein subunit

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000487

Protein Accession # AAC77114

CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGCGCACGGCAAATCCGAATGCAAAAATCGCACTAATCTCAAAAGTATACCCGATGCGTAGCCATACCGT
TGCTGCAGAAGGGGGCTCCGCCGCTGTCGCGCAGGATCATGACAGCTTCGAATATCCCCNNNCCCCCGTACTA
GTCGACGCCGTGAANANNNN

49G9-3 (12X)

fliP gene - putative structure; surface structures, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

AACGTACCGGATCCGG

GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCAGAC
TGGCGAATATCGGCCCGTTGCGTNCTACTCNACNCGTGCCNATGCGCATTTTGTCTCCNGCCTACGTGA
CCAGCGAGTTGAAAACCGCATTTTCAGATACGGCTTCACAGATTTTCATCCCTTTTTTGATTATCGACCT
GGTGATAGCCAGCGTGTTGATGGC

51B12-3 (6X)

flhM gene - flagella gene, flagella biosynthesis; motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

ATGAAAACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACTCAACTTCCAGCGGATTAATCGCCTTCCAGGCGTCGCTATAGCCTTCAAGCGCCAGTTTCAACATG
CGGTTGATGACGCGCTGTTCCGGTATGGGTAAACTCGCGACCTTCCACTTTGGTCGGGAAGCGTCCATC
GCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAGAA

57E7-6 (7X)

flp gene - flagella gene, putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCAGA
CTGGCGAATACCGGCCCGTTGCAGGGACCTGAAGCCGTGCCGATGCGCATTTTGTCTCCCGGCCTACGT
GACCAGCGAGTTGAAAACCGCATTTTCAGATAGGCTTCACGATTTTCATCCCTTTTTTGATTATCGACCT
GGTGATAGCCAGCGTGTTGATGGCATTGGGGATGATGATGTT

61G2-3 (10X)

255 bp down stream of flhB gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834

NGNNNATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATTAAGCGTGAATGATGCCAGAGCGCAAAGCGTTCAATGGTTTGAGTAAGGGGCAAAACAGGCGGG
ATTTAGGGCTTTTGTGCCACATATCCNNNNNNNNNGTACTAGTCGACGCGTGGCCA

63A9-1 (4X)

rfaQ gene (complement) - enzyme, macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

AAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATGTGTACCGTGATTGGCGCTAAGNGTGNGAAGCTTTTTTTTCCAANTACCATGCTTGCCNNATGACC
ATAANGTTGCGATATNTTCATTCCGTGCATGCAAACANCGTACCNNCAGCGCCACCATNCAACTGATG
CGTCNGANTAATGACCAGGTTNTANTTATTCTNTCGCCGAGCCTCATCANCNAANGCTCNCTTTNTNN

NCGGN\NNNNNATTTTNCNCGTCTNNNTNTTGNNTNANTNNNTTACGCGGCNACNNATTNGTTNTGG
TCNTACGNCGCNNNATAACNCGCNCNCTCNCNNCC

64F2-1 (9X)

factor Sigma32 – promoter dnaKp2; documented +1 site at 12121

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D10765

Protein Accession # BAA01595

CGNCGGATCCGG

GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG

CGTTTCGCCCCATTACAGACTCACAACCACATGATGACCGAATATATAGTGGAGACGTTTAGATGGG

TAAAATAATTGGTATCGACCTGGGTACTACCAACTCTTGTGTAGCGATTATGGATGGCACCCTCTCG

CGTGCTGGAGAACGCCGAAGGCGATCGCACCACGCCTTCTATCATTGCCTATACCCAGGATGGTGAAA

CTCTAGTTGGTCAGCCGGCTAAACGTCAGGCAGTGACGAACCCGCAAAACACTCTGTTTGCATGATAA

CGCCTGATTGGTCGCCGCTTCCAGGACGAAGAAGTACAGCGTGATGTTTCCATCATGCCGTTCAAAAT

TATTGCTGCTGATATCCNCCCCCNG

66F4-3 (10X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

TACCGGATCCGG

GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG

CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTTCGGTATGGGTAAACTCGCGACCTTCCA

CTTTGGTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAG

AACACCACCAGCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTTCAGGTTGGTCGGCACCGGCAG

GTTGCGGGCAAATT

67C8-4 (6X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NNCGTNCGG

GATATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG

CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCGGAA

ATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTCCATGT

GGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTCAGCATGATCGAGCCGCTACGGG

AATTGTTGGTTAACCCGCC

67C9-6 (8X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

ANCCGATCCGG

GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG

CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTAC
GTGCGTTCGGAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATT
GTGGTTAACACGCCGTTCCATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATC

67E10-5 (6.5X)

flil gene – Enzyme, flagella synthesis; surface structures, flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CACCTGCATTTCGAGGAGCGGAGAAACATCCGCCGAGCGGCAATCACCCTGAGCGTGCACGCCCTTCGGC
ACCGAGGATGTTCTCAATAAAATCTTTTACTTCGCGCCACGTTTACCAATCAAACCCACGACAATGATATCCN
NNNNNNNGTACTAGTCGACGCGTGGCCAAT

70G12-5 (5X)

flil gene – flagella synthesis, enzyme: surface structures; flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

TANGAAAAACGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCCAGCCCCTGGAGAGACGCTTNCCAGTCCGCGCGTTCAAAAATGCCTTGTTGCAAATAGCCCTCCAGCTG
CGGCCACAGGGCGATGGCTTTATCGAGCATCGGATCGCTGCCTTTGGCATAACGCGCCGACGCTAACCCAGATCGC
GGTTACGCTGAAAACCTCGACAACAGCTGTTTGAAGGTGCGCACTCGCGCGTAATGTTGCTCACTGATCAACGCC
GTCATTGCGCGGCTGATCGACGCTTCAATATCCNNNNNNCENNNGTACTAGTCGACGCGTGGCCA

71A4-3 (10X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP_418089

AGCNCGCCGGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAGGCCATTTGAAAAATCCTGGTCATAAAGATGCGATATCCCCCACCAGCGTAC
TAGTCGACGCGTGGCCANANANNNNNNNCGGCANNCCNCCCNT

74B5-2 (2.5X)

rfaG gene (complement)- enzyme, macromolecule metabolism, LPS; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

ATACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGCATTGCATCAACAGTTGCCGCACGGGGCCACCATGTTTCGGGTATATACACAGTCGTGGGAAGGCGA
TTGCCCCGAAAGCATTGAGCTTATTCANGNGCCAGTTAAGTCCCNACCAACCATGGACGCAATGCAG
AATATTATGCCTGGGTACAAAATCATNTNAAACAGCNTCCCNACAGGATCTGTGTGCGNNGNGTTCAATT
ATTATNCCCTCGNCGGATTATCTTATTTGCCTGCTNAATGTCNGTCTTCTNATTCCTAAATNT

76F11-2 (5.5X)

flhM gene - flagella gene, flagella motor switch biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NGAAAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCGGAA
ATGCAGGTGAAATTTACCAATATCACACCTCGCCGAACGACATTGTGGTTAACACGCCGTTCCATGT
GGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTCAGCA

77A5-2 (11X)

b1936 gene - orf; unknown function; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC 000913 (genome)

Protein Accession # E64957

CNCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ATTCAGGTGCGTAATAAGCTGGTGGCGCGTATCAGGAAGTGATGAGCATGCAGGTGTAGGTTTTGTA
ACCTGTTGTTAATTACATCCGATCTCACCGCGTGGGGCATGGATGGGGCAAACCTCACTCAATTTCTGGT
TTAAATGGATACCTGATCCTGAACGTTTTCTGCCATCCACGATCCGTATACGCGATAACCCCCCTGAA
CATCAGAGCGTCTCA

78E3-2 (7X)

fliA (complement) - flagella biosynthesis, alternative sigma factor

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74989

NAAAACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGGTTAATACCAGTTTTTCGCGCTCCGGCAACGTTTCGATGGCTTCCATCACCCGCTGGCGCAGATTAC
TGTCCAGTAGTTGTTGTAGCGGGTTTTCTCGCTGATGATCATCAGTAACCAAGTTCGATGCTATCGCCGT
GCTCTTCGCGCCACTCATCGTAGGAGAAGAGCTGGCTGTTATTGGTGTGAGCAACATTTGGCGATAA
TCGGCAATATCNCNCCCCCCCCGTACTAGTCGACGCGTGGCCAA

78F6-3 (2X)

tolA gene - membrane; colicin-related functions; membrane spanning protein required for outer membrane integrity

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000177

Protein Accession # AAC73833

ATACNCGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTAGCTGCTGCCAACGCAGCCTGACAAAGTGCGGGATCGCCACCTTCAGGTTTGATATCCAGTAA
CATAACATCGGGTGCCAGTTTTATGCGCAGCGTACAGGTTTTGCCTGCATAGGACGATGCGTCATAGA
ACTTACTTTTCGATAGCAGATTTAATCTGCCCGGCATAGTTATTGATATCCNCCCCCNNGTACTAGTCG
ACGCGTGGCCANNTATTNCGATATCNCNCCNGCCNGTCTANTCCNCGTGGNCATATCTGATNC

85G11-1 (6.5X)

Between 2 promoters (complement) - 1) factor sigma 70; predicted +1 site at 201135 and 2) factor sigma 70; predicted +1 site 2011238

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D89826

Protein Accession # AAC75005

ANNGNAANAGCNCGCCGGACATCCCGGATCCGG
GATCATATGCACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTCTTGNTCCACTTTGCCAATANCGCCGCCNTAGCNCTAGNCGNCGCACGNNCAGACGCGTGGCCA

89A8-3 (6.5X)

fliG gene - flagella structural; flagellar motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

CGNTACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCGGCTCCTTTTCAGCGCGATCAACAGCGATTTCGGAATCCACTTCCTGCAACAGACGCTGAATGCT
GCGATCGTCGACATCCACCAGATTCTCGAACAGGAACATCTCGTCGATGATTTTCTGCGCCAGCTCGCC
GTCGAATTCACGCACGGCGGTAATAACGGCTTCTTCCTGCTGAGTTTTC

92G7-3 (3.5X)

rnhB gene - enzyme; degradation of RNA; product is RNase HII, degrades RNA of DNA-RNA hybrids

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

GGAAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCAGCGCCGCCNTTNNNG
CGTCACGCGTNACTTTCGCCAGGATAGACGCGGCACTGATTTCCGGTACGCGGCTATCGCCTTTCACCA
CAGCCATCGCAGGCATCGGTAATTTCCGGCAGCGGTTACCATCAATCAACACATATTCGGGCGCAATA
TGCAGCCCAGCGACGGCACGCTGCATCGCCAGCATGGTTCGCATGAAGAATGTTTCAGCTCGTCGATATC
CNNNNNNCNCGTACTAGTCGACGCGTG

92G9-1 (3.5X)

rnhB gene - same clone as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

TANGAAAAAACGTTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCNCCNCCNNGTACTAG
TCGACGCGTGGCCAAATATNNNNATATNNNNNNNNNNNNNNCTANNNNNCNCNGGNNANNNN

94G6-3 (4X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP_418089

NNNGNAAAGCCCGCCGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAGCCATTTTCGAAAAATCCTGGTCATAAAGATGCGATATCCNGNNNCCNNGTAC
TAGTCGACGCGTGGCCAAAANNNCNNNNNNNANNNCNATNCTNGCNCCCNNCCANC

98E7-4 (6X)

fliR gene - putative enzyme, surface structures; flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

CGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACTGAATCTGGCATTAGGTTTACTTAATCGTATGGCCCCGCAATTATCCATTTTTGTTATTGGATTTCCATTAA
CTCTGACTGTCCGCATCTCTTAATGGCGGCATTAATGCCGTTAATTGCACCTTTTTGCGAACATTTATTCAGTG
AAATTTTAAATTTGCTGGCTGATATTATTAGTGAATTGCCATTAATATAATTCCGTAACGTTTATCATGTTATCCT
AAGGATTATCCGAAAAATAACCTACGAACATCTTCCAGGATACTCCTGCAGCGAAATATTTGTTTTAAGCTC
ACTCACATATCCCNNCCNCCNGTACTAGTCGACGCGTGGCCA

98E11-3 (5X)

flgH gene - structural component, surface structure; flagellar biosynthesis, basal body outer-membrane L (LPS layer) ring protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74163

AACNAAACGGNTNCGGCATCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAGC
GCTGCGCATACTTATGCCATATCCNNCNGNNGGTACTAGTCGACGCGTGGCCANATTNNNNNATCNN
CNNNNNNGGGGCGNN

98G12-4 (5X)

mdoG gene - enzyme, osmotic adaptation; periplasmic glucans biosynthesis protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000206

Protein Accession # AAC74132

AAACGACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGGGCAAGTTGCTTTTGGGCGTCTCGTAGCCTTTCCCGGCTAAAGATTGAGCTTGCTTTGCGACATCAT
CAATACTGAAAGCCCAGCTTGAAGATGTATACAGGGTTAACATTACTGCAGCACTCAACCAACGCATT
TTCATTATTTGTAGCTTATGTTTCATAATTAGTAAGGCACTTCCCCCTTTNGTGTGCTTATATCCCTNNG
NTNCCNTNCTAGTCNACNCGTGGCCACTNCTATCCNGNNNTCCCCGNTNNGCAGTANTCAGAC

103C8-4 (9X)

fliP - flagella biosynthesis, surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

GANNAAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCCTTTTCCAGCGCCTCCTGCATTGATATTTTCTCTTCGCTGAATGGCTGGTACGCATCTA
CATAAATTTTGTGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGCAATACC
TGGTTAGGTGGCGCGGAGGGTGTTCACGCGCGTTACGCAATAAACCAAAAACAATGATGATGCGGG
TGAAACTGGTCATCATCAGTAAATTTGCCGGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGC
ACCGGGAGCGACCAGCTTTGTCCACCGCCAGGCAGCG

103E8-4 (7X)

yojN - putative regulator, not classified; product is putative 2 component sensor protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000310

Protein Accession # AAC75276

NATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTGCAACCTGTATCACACCCGATGAAAGATTAAATTAGTCAAGATTATGATATCTTTTTAACGGATAAT
CCGTCTAATCTTACTGCCTCTGGCTTGCTTTTAAGCGATGATGAGTCTGGCGTACGGGAAATTGGGCCT
GGTCAATTGTGCGTCAACTTCAATATGAGCAACGCTATGCAGGAAGCGGTCTTACAATTAATTGAAGT
GCAACTGGCGCAGGAAGAGGTGACAGAATCGCCTCTGGGCGGAGATGAAAATGCGCAACTCCATGCC
AGCGGCTATTATGCGCTCTTTGTAGACACAGTACCGGATGATGTTAAGAGGGCTGTATACTGAAGCAGC
AACCAGTGACTTTTGCTGCGTTA

104G4-5 (2.5X)

Between mreB and yhdA genes (complement). mreB: phenotype, cell division; regulator of ftsI, penicillin binding protein 3, septation function. yhdA: orf, function unknown, hypothetical protein, 1232 bp upstream of mreB

Transposon Tn10 Accession # AY528506

Nucleotide accession # M22055

Protein Accession # AAA83892

ANNNNCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCANAATCATTAGGGGATTNATCAG
CTNAATGCATGCNCNACCATTGCCTCNGCTGTTTGCAACCGNGTAAGGNGCATTTCATNTGCATATGTT
GCTGCNANCAATCTGGCTGAGNAGACAAGCNCACCTCCCATGANACGCATCGCGCATTATTNTACGTGA
AANCGGATNNAANGGNTGGNTAAACCNANGANCNNCGCCGANTATNNTCCNCTGNCANNCTNANN
TNGNCTNGNACNGANNNCNANNNCACNCCTCTTTNTNNNNNTCCGNTNNGNNGNNNNNNNTNGTNN
TCCNNCCTGTNTNCANNTNNCNNNGNTCNTNCNCCNTCTNTCCANTGCCANTTGTNNCNAGGTNCGA
TNTCTGCNGACCNACNNNNTAGNANCCNN

107B12-2 (2.5X)

Upstream of promoter - factor sigma 70; predicted +1 site at 3806141

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # AAC17834

GNAAANCCCGCCGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GCGGTAGCGTGCTTTTTTCTGCTTAACCTTAACCAGACAATCACACAAAAGAGTCGCTAGTGGAAGAGC
CATTTGAAAAATCCTGGTCATAAAGATGCGATATCCNNNNNNN

110E8-3 (6X)

flp gene - Putative surface structure, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

AACGCTNCCGATCCG
GATNATATNAACAGATNTGTATNCACCTTATCTTAATGANATTTTACCANAATCATATTGGGGATATCATAT
ANGGGCTGCCCCCTTTTTCCAGCCCCCTACTGCATTGATATTTTNTCTTCGNTGNATGG
CTGGTACGCATCTACATAANTNTTGACGATCACCGGTGACNTAATAAAANAGGNCN
NANNCANTGCCANTCCCAGCAATNCNTGGTTNNGTGGNGCGGACGGTGCTNCCATN
GCNNGACNCACNNAACCNANNNCNATGANGTNCNCNCGANANTGGANATCATCC
TGCAANNCNACNGNATNCNNA

110F12-2 (9X)

Between flhD and insB_5 genes (complement)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834, AAC74963

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGATNANCTGCAATAAGCAGAACCCCTTTTTGGNTTAATATGTCCTTACAAATAGAAATGGGTCTTTACACTT
ATCTAAGATTTTTCTATATCNCNCCNNGTACTAGTCGACGCGTGCCATTTATNNNNNATNTCCTNNTNG
TCTCNNGNNCNNCNCGCGGCCNCANCNNAATATNNNTNNNNCNCNTNCACTCTN

111G8-1 (4X)

flgK gene - structural component, flagella biosynthesis; hook-filament junction protein 1

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000209

Protein Accession # AAC74166

AACCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGGGTGGCAATGGTGTCTACGTTTCTGGTGTGCAGCGTGAGTATGATGCGTTTATTACCAACCAG
TTACGTGCGGCGCAGACGCAAAGTAGCGGTCTGACTGCCCGCTATGAGCAGATGTCGAAAATCGACA
ATATGCTCTCCACCAGTACCTCTTCGCTGGCAACACAGATGCAGGATTTCTTCACCAGCCTGCAAACGC
TGGTGAGTAACGCGGAAGACCCGGCAGCGCGCCAGGCGCTGATTGGGAAATCAGAAGGATTGGTGAA
TCAGTTTAAAACACCGATCAATATCNCNCCNCCGCTACTAGTCGACGCGTGCCCANANNATNCT

115A3-5 (2.5X)

fliD gene – flagella biosynthesis, surface structure; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

ATACCGATCCGG
NTCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GCTTACGCCTGCTTTTTCGCTTGTGATGGCATCACGGATCCCGCTTAACGATGAGTTAGCCGCGCTGAT
ATCAATGGTNATCGTACTANTCGACGCGTGGCCATGAATGGTGAGTTTACTGTCGCTGGTGGCGATCG
CCGTTTTTCATATCGNCNNTTNCNGTACTAGTCGACGCGTGGCCAAATTNNTNTNANAAAAATTCTN

115B7-6 (7X)

flgB gene – flagella biosynthesis, cell-proximal portion of basal-body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

AACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCGCGATATCGATTTTGCCAGTGAACCTAAAAAAGTCATGCAACGTGGACGGGATGCAACCAGTGTG
GTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGCCTCCTACCGCAGAACT
GCAATACCGTATTCCGGACCAGCCTTCGCTTGACGGTAATACCGTCGATATGGATCGCGAACGCACCC
AGTTTGCCGATAACAGCCTGCAATACCAGATGAGCCTTAGCG

122F6-1 (4X)

fliL gene - flagella gene; putative surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75011

CGNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACGACGCGTTGCTGCGCTTTGTCGTCAGCGGCAACCTGATGCGAATGCCAGTAGCTGTAACCTGCGC
TGGCACAGGCCGCGAGGGTAATGAATACCAGAATCGGGATCCAAAGCGATCGCTTCTTCTGCTT
ATCGCGTAATCAGTCATGTGTTGCGGTCTTCCTGTGTCGCTACTGCTTATC

123B8-4 (3.5X)

rfaQ gene (complement) – Macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTAAGTGTGTGAAGCTTTTTTCCAAATACCATGCTGCCGATGACCATAAAGTTGCGATATTTTCAT
CCGTGCAGGTAAACAACGTACCAGCAGCGCCACCATCCACTGATCCGTAAGATTAATGACCAGGTCAT
AATTATTCGCACGCAGAGNTTTATCAACNAAAGCACATTTTTAATTTNATCGAAAGTTCCNCNCCTT
TATTGCTTANCCCATAGAGCGCANTNNTTTCGGGTTTNCANACAAAATNTGGATGGTGNCCTGNCNA
AGCNNCANGTCTANNTNNGCTNTATGAGAATCTG

123E4-3 (6.5X)

fliR gene – putative enzyme; flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTACCCGTTTTCCGTACGCTGCGTTCGATCAGAAATCGGCGCGGTGGAGATCATCGCCAGCTCNCGC
ANTNACGGNCAGAAANTACAGGTTTAACCAAGGATAGCCATTGTTNGCTTGCCACCTGCANCATAGTACG
GTTACCCNATGATTTTACTNGNAGGTTAGTGAACAANGTTCGGNCAGTNATTCAACAACACATTNNGCA
TGNTCTGTCTNGGCANNTATTTTGGTGATNAANANGGCCGATNNTTTTNCGANTNNCCGNNNTGGGNT
NCTTNTTCATCNAGTNNCANNATGGGCGNGTATN

125C9-2 (7X)

fliP gene – Putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

TACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCCTTTTTCCAGCGCCTCCTGCATTGATTTTTCTCTTCGCTGAATGGCTGGTACGCATCTACATAA
ATTTTGTCTGATCACCAGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGCAATACCTGGTTAGGTG
GCGCGGAGGGTGTTCAGCGCGTTACGCAATAAACCAAAAACAATGATGATGCGGGTGAAACTGGTCATCAT
CAGTAAAATTGCCGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGCACCGGGAGCGACCAGCTTTGT
CCACCGCCAGGCAGCGCTGGCTGGTGATACCCGGCAGTTGCGCGAAGGCGAGGGGCGTAATCAGCCAGAGA
AGGACAGGTGCGACAGACAATAAACGACGCAT

125F2-4(3.5X)

rfaQ gene (complement) – enzyme; macromolecule metabolism: LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

GNGNAAAAACGTNCCGG
ATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGTGTCTGATAAAGCAGCATATCGATTTTTGCATCANGATAATTCTGCTTGAGCGTACTGATGAC
AGGAGTAGTTAATAACATATCCCCATGATATCNCNNNNCNGTACTAGTCGACGCGTGGCCA

126G2-2 (7X)

flhA (complement) - flagella biosynthesis; possible export of flagella proteins

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74949

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTGGTG
GATACGCGGACGCGAACAACAAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAATAATACC
GTTGTCTGAAGCGACGTGGAACGATGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGGTTAT

GGACTGATCCCGATGGTTCGATTTCCAGCAGGATGGTGAGTTGTTGGGCCGTATACGCAGTATCCGCAA
G

126A3-2 (7X)

flhA gene (complement) - flagella biosynthesis, possible export of flagella proteins

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74949

ACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTGGT
GGATACGCGGACGCGAACAAAAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAATAATAC
CGTTGTGAAGCGACGTGGAACGATGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGGTTATCGAC
TGATCCCGATGGTTCGATTTCCAGCAGGATGGTGAGTTGTTGGGCCGTATACGCAGTATCCGCAAGAAA
TTTGCCAGGAGATGGGATATCN

132B8-2 (7X)

fliM gene - surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NTNNAAAAACAGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTTGCCC GCCATTTTCGTATGGGGCTGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNCCNGG
NGCGTACTAGTCGACGCGTGGCCAANNNNNNNNCNCNCTAGCNNTAAAANNNGNCATNANCCNCNC
NCACAANCACNNANGNANNCNTTNCNAAACNANCGTANNATANCCCCNNC

136E3-1 (7.5X)

arcB gene (complement) - enzyme, Global regulatory functions, aerobic respiration sensor- response protein; protein kinase/phosphatase, sensor for arcA

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000400

Protein Accession # AAC76242

NNAAAGCCCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCAAAGCCTGCTTTGANATCCGTAAAGNGCGGACTAANCNACNCGNGGNCNAA

139G5-3 (5X)

rfaP gene - enzyme; macromolecule metabolism: LPS; phosphorylation of core heptose, attaches phosphate containing substrate to LPS core

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000440

Protein Accession # AAC76654

GNAAAAAAGCNACCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTAAATCCATTAACTCGCGCATCATTTATTATTACCGAAGATCTCACTCCCACAATTAGCCTTGAAGATTATT
GTGCCGATTGGGCAGTCAACCCGCGCTGATATCCNGNNCNNNNGTACTAGTCGACGCGTGGCCATANANTNAGC
TCNTNCTACNCCNANTCCTATCCACCCGTGGCTNCAGNNANCATTTCNGNNNACACCANTTACNNNCCAGNC

CNCNTCCCCCNGNNCTCNNCTACTCANNACTTCANNANANNATGNCNTTCNNNNGCNNNTCGNTCNCCCACNA
CNNCNTTTNTTNCNNCCTCTNNCNANCTCNNCCNTNNCNCNTNTNATTCNCCTTTTACCCTNAN

152B4-6 (9X)

flgI - flagella biosynthesis, putative surface structure; product is homologue to P-ring of flagella basal body in Salmonella

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74164

GNNGAACGNCGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CACTTTGCATTGATTGCAGTATGGACATCAGATCCATCGGCGTAGCGCCCAGCGCATTGAGCGCGCGC
ACCACGTTATTGAGGCTGGCGCTGGAACGTACGCTTTGCAGCGAACC GCCGCTCTGGCGTAAATCGAT
CTGCGTTTGTGGAGTAACCACAGTCTGTCCACCACCAAACGGTGTATCTGGCTGGCTGACATTGGCCTG
ACGATTAACGTGTTACTGAGAGATTCCCCTGCGCTACCGCGCAGCTGTCGAGGGTCACTTCGCGATTTCAT
CACCACCGAACCGGTGCGCGAGTTAATCACTACTTTAGC

163E7-5 (4X)

fliD gene – flagella surface structure; capping protein (same clone as 1B10)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

TNGNAAAAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTACCGCCGCGCAAAAAGCGACGCTNACCCCC
ATTTCAAATCAGCAATCGTCGTTTACCGCTAACTTAGCGCCTACGGTACGCTGAAAAGCGCGCTGAC
GACTTTCCAGACCGCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCAGCACCACCAGCAG
CACCACCGCGTTCACTGCCACCACTGCGGGTAACGCCATCGCCGGGAAATACACCATCAGCGTCACCC
ATCTGGCGCAGGCGCAAACCCTGACCACGCGCACCACCAGAGACGATACGAAAACGGCGATCGCCAC
CAGCGACAGTAAACTCA

163F3-5 (8X)

fliD gene – flagella surface structure; Capping protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

NNANNAACAATACGTCC
CAAGNANANNTGACNAGANGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCNG
GGNCCGGTCTGGATTTAAGTTTCCATCCTTGATAGCCTACCGCCGCGCAAAAAGCGACGCTAACCCNC
CATTTCANATCAGCAATCGTCGTTTACCGCTAACTTAGCGCCTACGGTACGCTGAAAAGCGCGCTGA
CGACTTTCCAGACCNCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCANCAACCACTGCA
GCACCACNGCGTTCACTGCCNCCNCTGCGGGNNAACCCATCGCCNGGAAATACCCCATACCGNTCAN
CCATCTGGCANATGCNGCNAACCCTTGAACACGC

167C2-3 (8.5X)

flgB gene – Structural component, flagella biosynthesis ; cell – proximal portion of basal body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

AAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCAATCTGCGCGCCAGCGTCAGGAAGTGCTGGCAGCAAACATCGCCAATGCCGATACCCCTGGT
TATCAGGCGCGCGATATCGATTTTGCCAGTGAACCTAAAAAAGTCATGCAACGTGGACGGGATGCAAC
CAGTGTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGCCTCCTACCG
CAGAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGA

Sequences of Down Mutants

1G3-6 (16X)

ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_415541

ATAAAACGGNTACCGGATCCGG
GATCATATGACAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATGAG
GGCGCTGTTTCCACAGCCCTTTTAACGTTTCAGGCATTAATATCCAGCACAGTGNCCTNGNNNNCNCNNNNNC
NTCCACTGATTCAACTGCAGCTTCCAGCTAATATCAATATCTTCGGTGATCATATNAGTCCACNCGGNNCTAGT
CGACGCGTGGCCANNANTNNNNCNTNTTTNTNNTN

11E4-3 (12X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA (Not Available)

Protein Accession # NA

TTTAAAAACCGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCCAGGCGTCTTTTCCGGCCATTGTCGCAGCACTGTAACGCGTAAAATAGTGCTTTCTCTTACTCTTCTGGCTG
GACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCNNNNCNNNNGTACTAGTCGACGCGTGGCCANANN
ANTNNTATNTTTNANNACNN

12F12-6 (23X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

TTGAAAACCGCTCCGGATCCNG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTAATTCTGTGGGATATC
CNNCCNNNCGTACTAGTCGACGCGTGGCCATNTNACNTNCNGCAATNCNTTCTGACACTTCNNNTNCTNTNN
AT

14B7-4 (4X)

leuO gene -putative regulator; probable transcriptional activator for leuABCD operon; amino acid biosynthesis:
Leucine

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

GCNNGCGGTAAACGNCCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG
AGTTAAGTGTGACAGTGGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGT
TAAGCAAACCAACANCTTNCGNATGGNCGATTTCAACTTATTAACNCGTTTCGATGCCNTGNTGNAGGA
GCCNANCATTNTTNCAGCCCGCTCATCGCCCTGGGAACCTTCNCCCCCCTNCNTTCTNTGCTNGCC
TTGGGGCCCCCNCACNCAACGNAGACNGGGCCNATCCC

16C8-2 (24X)

Promoter (factor sigma 70, predicted 1+ start site 1986220); upstream of b1904 (orf, unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AACCGTACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG
TGCNACGNCNCTNTNANNNCCATNGATNTNGCACTGTAACGCGCTAAATAACGCTTGTNTCTTACTCT
TCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCNCNCCGTACTAGTCGAC
GCGTGNCNATATTATGNNNNCCNNNNNCTANTNNNC

24E12-4 (8.5X)

fucA gene (complement) - enzyme, degradation of molecules: carbon compounds: product is L-fucose-1-phosphate aldolase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC75842

CNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAGAG
GCAAGTGTCAATAATCTGACGAGCAAGTTTATTTTCGTTCCATTAGCTACCTCTCTCTGATTCAAAACAG
GGCAATAATGTTGTTCCCTTTCACACTATTGAATTAGCCGTTTAATTACCCACCATCTTCTCCTGATTAA
CAAGAAAGAAATTCACAAGCTTATAT

26G11-3 (8X)

ycdS gene - (complement), putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC74109

AACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG
CCAGATGCGTTTCCTGACCCTCAAGTGAGACTTCATGACGCTGGTTACTGTGCGAAAAATCAGTGAAAG
CCCAGGAGACACCGTACTTACGCCGCTCATTGATACAGCGAACATAAGCCTGAGCACTGTTGCCT
GTAACACCATTTTTTTCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCCAGTTGCGAACCAATACG
CCAGTTATCATTAATAATCATACAGCCAGACAGGCGCGCGCGGGTTTATGCTCATGATTGAAAACGC
GTTACGCGTACTCTGCCTCGAGCCAGATATTACG

27F9-2 (2X)

Between promoter (factor sigma 70 predicted 1+ start site 4272977) and yjcC gene (orf, unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG

TGCCCAGGGTTTTTCACCTTGCAATGGCCGGGTATAAACAGGCAGGAAATTGANANCANTGAGNCATN
NNCNACGANACCAATTNCTGGCNTNGCCGGGCATTATCTTTTAAATTCTCTTTCCCATCATTCTTTTCGCT
ATGGATTGCCTTCTTTGGGCAAAATCAGAAGTGAATAATCAGCTCCGAACCTTTGCTCAACTGGCACT
GGATAAATCCGAGCTGGTCATT

31A4-4 (7X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCTTC
ATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCATTATTGACTGTGCTTTTTT
CGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATTTGCCCGG
TCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAACGCGCCAAGAT
GATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATG

31G6-3 (2.5X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AAACGACCGGACCG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCNNGCGTNTTTNCCGGCCATTGNCNCAGCACTGNNACGCGTAAATAGNGCTTTCTCTTACTCTTC
TGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCCCCCCCCG

32A4-2 (14X)

Between ptrB & yebE (complement) - ptrB gene - protease II; yebE gene -unknown function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

NGANNATACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTTGAAACATCTTATAAGGGGTGGCAAACTCACCGGGGATGCAAGCGAAACAGGGGAGTCATTGCT
TAGATGATGACAGGTAATGGCGCGGATATCGAATGTTATGCAANCAGANAANANCAGNCTGTTCAAA
TGGCTGTGCGATTCTGGATAGCCCGAAATAGTCAACTTCAGGCTATCCAGAGAGCGGAATTATTCCGC
CAAAGTGCGTTTTTGTGTTGAGATCGCGTTCAATGCCGTCACGAACATCCTGGGGGATTTTCAGCGC
GTCACCCAGTGCAATCAGGTAATGCGTTCCATAAAATGGTCAATATCAATAGCCGCGNNACTAATNN
ACNCGNGGCCNAGCGCCTCTTC

35C6-2 (6.5X)

hscA gene (complement)- factor, chaperone; product is heat shock protein chaperone, member Hsp70 protein family

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000339

Protein Accession # AAC75579

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGACGGTCTTTTGTAGCGTGACGGCGATGGAGAAATCCACCGGCGTTGAGGCGTCTATTTCAGGTCA
AACCGTCTTACGGTCTGACCGATAGCGAAATCGCTTCGATGATCAAAGACTCAATGAGCTATGCCGAG
CAGGACGTAAAAGCCCCGAATGCTGGCAGAACAAAAAGTAGAAGCGGCGGTGTGCTGGAAAGTCTGC
ACGGCGCGCTGGCTGCTGATGCCGCGCTGTTAAGCGCCGAGAACGTCAGGTCATTGACGATGCTGCC
GCTCACCTGAGTGAAGTGGCGCANGGCGATGATGTTGACGCCATCGAACAAGCGATTAAAAACGTAG
ACAAACAAACCCAGGATATCNCCNNNNCNGTACTAGTCGACGCGTGG

37B5-2 (11X)

yedK gene - hypothetical protein, function unknown

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74998

NGAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CTCCGCGCCCTGGTTTTTAACATTACCCACCGCGCGCGATATCNNNNNNNNNGTACTAGTCGACGCG
TGGGCCAANTANNNNNNCNNNNNTNNNNNNNTNNNNNNCGNNTNNNGNNNNNCNC

41G10-2 (10X)

leuO gene - putative reg of AA biosynthesis (leucine) - Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGTT
AAGCAAACCACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAGGAGC
AAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCNCNGTACTAGTCGACGCNGN

41B10-5 (9X)

leuO gene - same as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGTT
AAGCAAACCACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAGGAGC
AAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCNC

44C2-1 (10X)

yedS gene (complement) - same clone as 31A4-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG

GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCTTC
ATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCATTATTGACTGTGCTTTTTT
CGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATTTGCCCCG
TCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAACGCGCCAAGAT
GATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCT

46E5-5 (10X)

ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GAGCTGGNGCGTTTCTCCCCACGGCCAGTGGCGTTCACNATAGACCCAGAAATAGACGCCGNCNACAATNCA
CATAATGGACATAAAAAACGGCCAGAAGAAAACGAACCTNATCATCAGTTCACCGAGTGAAAGTACGCTACGC
ATAGGGGTATGCATAACACCAGACATAATATAAAAAACGATACGATGCGATTAA

48A4-5 (20X)

trs5_11 (complement) - IS, phage, Tn; transposon related functions, IS5 transposase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000427

Protein Accession # AAC76530

GAGATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCCACCCTGGCCGATGCTGGCTTTTCATGTATTTCGATGTTGATGGCCGTTTTGTTCTTGCGTGGAT
GCTGTTTCAAGTTCTTACCTTGCCGGGGCGCTCGGCGATCAGCCAGTCCACATCCACCTCGGCCAGCT
CCTCGCGCTGTGGCGCCCCCTTGGTAGCCGGCATCGGCTGAGACAAATTGCTCCTCTCCATGCAGCAGA
TTACCCAGCTGATTGAGGTCATGCTCGTTGGCCGCGGTGGTGACCAGGCTGTGGGTCAGGCCACTCTT
GGCATCGACACCAATGTGGGCCTTCATGCCAAAGTG

49C2-1 (9X)

ycdS gene - (complement), putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GATGAATTACGGGCGATGACAGAGTCATTACCTGAAAATGCATCTACGCAACAATATCCCACNNANTN
GTACTAGNCGACGCGTGGCCATCAACTTGCTGCCGCGATTGACGATGCCAATTTAACGCCAGATATTC
GCGCTGATATTNCTANNCGACGNGCNGGNGACGCGTGGCCAANGCNNNNCNTNNNCTNNNAANNNT
GNNCNGNNCNTGGCTGNTGTCCNNNCTGNNANCGCCNCANAACNTCNTGNCNTNNNNNANGCTGNC
GTCCCTTANNGAAGNGGCCNNGGNNAAATNATGTNNACNCCNTNNCCAANGNTTNNNNACTNNACNA
NCNACCCNNGATNTC

49G12-3 (20X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCAATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTATTCTGTGGG
ATATCCNNCCCNCCCGTACTAGTCGACGCGTGGCCATGNNATNNNCCGNNATTCATNCTGATGACNCC
CCGNCAGTTTATANATATNNNNNNNNNNGTNCT

51A10-4 (2X)

modC gene – ATP-binding component of molybdate transport; Transport of small molecules: Anions

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73852

AACGCACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
ACTGACGCGCCCGCAAAAAGGGCGGATTGTCTCAATGGGCGGGTACTAAATGATGCCGAAAAAGGTATCTGC
CTTNCCGTACTAGTCGACGCGTGGCCACNNNTTCATTNCCNCTANCTCNNAAGTNNNCCNACTCCGNGNNCN
ACCNNCCNNNCCCNCTNGCAGNCNTGTNCNCNNACNNCGGCNACCCNNNGANNNCGNCTCCNCCCGCCCTNT
CNNCACCTNNNNANGGCNTACCNGCCCTCNGGCTCNGTTACCTTNNTNNNTNNCCGNCCCNCTCANANNCN
CCNTNACNNGNCNNNCNATNCNTCGCNNNNNAGTANNCCCNCTCCCCCACNCNCNNNCCGTNTTNNCNCT
TNAGANCT

56C11-1 (5.5X)

modC gene – Same clone as 51A1-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73852

AACGNACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
ACTGACGCGCCCGCAAAAAGGGCGGATTGTCTCAATGGGCGGGTACTAAATGATGCCGAAAANGGTNTCTTG
CCTGNCCCGTACTANTCGACGCGTGGCCAACNAACCTNCTTNTANNNTCGCNNTTCCCCCTTCNGCNCNTCNN
CCACTCCNGCTGCTCCTNCNNCCTTCNCGCNCCNTACCNTCGTNNCCTTANTCCACCTGCNNCTATCCNCG
GCCGNCCTCCCGNCCCCCNCTNCAANTNGTTCAAGNACNGNCCNCCCTCGCCCNAGCGCTNCCNGNGCCAG
NNNCTNTTCATNTCCCTCCNGATCCANTCNCNNCCNTTNCNCTCTNACNNNCCNGTCNCTNNCCCCCTNNTTA
N

62C9-2 (20X)

yecK gene (complement) - putative enzyme (cytochrome C type); not classified ,product homologous to
TorC cytochrome of TorCAD resp. system

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74943

CNCGACCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
GGTTTCGCTGTCTTTTGTGCTTTGTTATGCATTTTCTGCGCAGATTCACTTTGCGAGGCAATATCCATG
GCATCAAAAANAATGGCAACTACGGCACGTTGCAGAGTCAGTGGCTTTTAATTCTTTCCATACTGTTTCG
GCCATTTCTGCGCATGAGCTTCGAACTTATCGTCACTGTCTATTTTGCCGCTAACAAATTCATGATAA
ATATCTTTAGATGC

63E2-3 (2X)

between genes clpP and clpX – clpP: enzyme; degradation of proteins; ATP-dependent proteolytic subunit of clpA-clpP serine protease, heat shock protein F21.5. clpX: enzyme; degradation of proteins, ATP-dependent component of serine protease, chaperone.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AAACNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAN
GGTTTTGACCCATGACAGATAAACGCAAAGATGGCTCATGCANATTGCTGTATTGCTCTTTTTGCGGCAAAGC
CNNCATGAAGTGCGCCAGCTGANNAGCCGGNCCATCCCTNTATATCENNCCNNCCCTGTACCTNGNCGGNCCG
TGGNCCNNCTCCTNTCNTTNNCNTCTCCCNNTCTNNNNCCCCCTCTNNCGCGGNCCCNTGANNCGCCTCNCTT
CTTNTACCTCCNCGNGCCTCTACCNCTCGNNCCTCNCCCCCACCTCCTTATCCNCCCTCCTNTCNTTCCNTCTC
CACCTNTCCTTTCCNACCGCNCNACATNNNACGTCTCNTTCCCTNNNNCCACNNNTNATCCTTCNGCNCCCCTCNG
NGCGAANCNTCNCTNNNCTANCGGCNCGNTGNNCNTGCNNCNCANTNANCNCNCNCTNATTGAGTGCGNGT

66E10-1 (12X)

ycdS gene (complement) - putative outer membrane protein, same as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGATCCGG
GATATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GTGACGACATCCGTGCCATAATGTTTTTGCCAGGAGGCACCAACACCTGCGCTGAATATTTGCTCCCAGCTATT
TTCATAGCTTCGCCATAACAAATGGCTTGCTCAAATGCCGGAACAATATCNNNCNNNNNGTACTAGTCGAC
GCGTGCCA

68E11-2 (2.5X)

glnE gene (complement) – enzymes, translation and modification; Adenylylating enzyme for glutamine synthetase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000387

Protein Accession # AAC76089

AAACCCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTATCTGCGTCTGGCGCAACGCATTATGCATCTGTTTCAGTACGCGTACCTCTTCCGGCATTGTA
TGAAGTGGATGCTCGACTGCGTCCGTCCGGGGCGGCGGAATGCTGGTGACATCCGCAGAAGCATTG
CCGATTATCAGAAAAACGAGGCCTGGACGTGGGAACATCAGGCGCTGGTGCGTGCCTGTAGTGTA
CGGCGATCCGCAGCTCACCGCGCACTTTGACGCACTGCGTTCGCGAGATTATGACGCTGCCGCGTGAAG
GTAAACTCTGCAAACGGAAGTGCGGGAAATGCGCGAGAAATGCGCGCTCATCTCGGCAATAAACA
TCGCGATCGCTTTGATATCAAAGCTGATGAAGGGGAATTACCGATATCGAATTTATTACCCAAT

68A3-1 (>24X)

wcaI gene (complement) - putative enzyme, colanic acid biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_416554

GNCNNCTAAAAACNTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAN

GGCCGNNANGGTGTGGCGCTGCCCGCTGTATGTGCCAAAACAGCCGAGCACCTGAAACGCCTGTTGC
ATCTGGGCAGTTTTGCCGTCAGCAGTTTCTTTCCGCTGATGGCGCAACGTCGCTGGAAGCCGGATCGCA
TTATTGGCGTGGTGCCAACGCTGTTTTGCGCGCCGGGAATGCGCCTGCTGGCGAAACTCTCTGGTGCGC
GTACCGTGCTGCATATTCAGGATTACGAAAGTGACGCCATGCTGGGGCTGGGCCTTGCCGGAAAAGGC
AAAGGCGGCAAAGTGCCACAGCTGGCAACGG

73E6-6 (16X)

ycdS gene (complement) – putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CGCATCTGGTCTTACCATAATTTGATTGTGCGATTTCTACCCAGTCTGTATTACGAACAAAATACAGAA
CACGATACCCATACTACAACCTATAAAAACGTTTCGATATNGTCCGGCNGTGTGCTGCNCGNCNNGT
GGNCTGGCGAAGCTATGAAAATAGCTGGGAGCAAATATTCAGCGCAGGTGTTGGTGCCTCCTGGCNA
AAACATTATGGCACGGATGTCGTACCCAACTCGGCTACGGGCAACGCATTAGTTGGAATGACGTGAT
TGATGCTGGCGCAACGCTACGCTGGGAAAAACGACCTTATGACGGTGACAGAGAACACAACTTATAC
GTTGAATTCGATATGACATTCAGATTTTAAGGATAAATATGTTACGTAATGGAAATAAATA

73E9-1 (12X)

ycdS gene (complement) - putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

ACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CACCGTACTTACGCCGCTCATTTTGATACCANCGAACATAAGCCTGAGCACTGTTGCCTGTAACACCATTTTTCA
TTGCCCGTAATGGAACGCGGTGAGAGAGGGCGTTCCAGTTGCGAACCAATACGCCAGTTATCATTAATAATCATAT
CNGCCNGNCCNGTACTAGTCGACGCGTGGCCANAAATTGAAAACCTGGTTTGCCANAATTNTCTNGATCNCCTA
AAAAGCTATNACTGGACNCGNTATNATGGNTNTGNNTTATCTGGNANGGGGNNNCANAAAAATNCGNTGCCA
ATGGNTNATNCAATTGNCCATNAAATTAAAAACATCCCTTANGNTNAAAGACAAATNNATTTTNTAATTCANG
GGCNA

73F2-1 (12X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NNGNAAACAGCCGGACNTCCCGGATCCGG
GATCATATGACNAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTANGGGATTCATCAG
NCAGATGCGTTCCTGACCCTCAAGNGAGACTTCATGACGCTGGTTACTGTGCGGAAAAATCAGTGAAAG
CCCAGGANACACCGTACTTACGCCGCTCATTTTGATACCAGCGAACATAAGCCTGAGCACTGTTGCCT
GTAACACCATTTTTTATTGCCCCTAATGGAACGCGGTGAGAGAGGGCGTTCCAGTTGCGAACCAATACG
CCAGNTATCATTAATAATCATATCANNCCNGAAGAGGACTAGTCNACGCGTGGCCANNACANCCNCACT
NNTNAACNTGNGGCTACNANTNTACCGCCANNAGNNTTACNTNANTTNGCNCNCCTNCCANTCNC
NCCCNANGTNNNCNNAANCTNNANNCTN

75E11-5 (1.5X)

moaC gene - enzyme, biosynthesis of cofactors, carriers: molybdopterin; molybdoprotein biosynthesis, protein C

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000181

Protein Accession # AAC73870

NNAANATACGGTTCGGNTCCG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
ATGGAAGCATTAAACCGCGGCCTCCGTGGCGGCGCTGACCATTTATGACATGTGCAAAGCGGTGCAAAA
AGATATCNCNNCCNNNGTACTAGTCGACGCGTGGCCAAANATCNGGGNTCTCNNNNNTGCTNGCTNC
NAATCNANTGNACCCNCTNAACCCNTTCNAGCTAAACATNTNNATNTGNAACNNATAAACNCAGGAC
GNCACATATNGNGTNNACNT

84A10-6 (11X)

ycdR gene - orf, unknown function, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNNGANACGNCCGAATCCG
GATANTANACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCCGCTTTAA
AAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAAGCCATTCGCGGTCCACATAT
TAAAACTGCACGAAATATTTTGCACCTCCGGTAATACAACCTGAAAGTGAAGCCTGGTTTGCACAGA
ATTATGCTGATTTCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCTGGAAGGTGTCTG
CAGAAAAATCGGCTGACCAATGGTTAATACAATTGA

86E7-6 (10X)

ycdQ gene (complement) - orf, unknown, putative enzyme homologous to IcaA in Staph

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGGATGCGGCGGCATATATTGTGGAACCGAT
GTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTGGTGGG
TAAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATCTATGGAA
ACGTATTTACCGTTT

86F11-6 (11X)

ycdQ gene (complement) - same clone as 86E7-6

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGGATGCGGCGGCATATATTGTGGAACCGAT
GTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTGGTGGG
TAAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATCTATGGAA
ACGTATTTACCGTTTCC

91F9-6 (2X)

b2531 gene – orf, function unknown; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_417026

CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACAAAATCATTAGGGGATTCATCAN
GGGCCCCGGTACCGTTGGCTGATATTTCCGAACGTACAGGAATTTCCCTTTCTTATCTGGAACAACACTGTTTTCCCG
TCTGCGTAAAAATGGTCTGGTTTCCAGCGTACGTGGACCAGGCGGTGGTTATCTGTTAGGCAAAGATGCCAGCA
GCATCGCCGTTGGCGAAGTAATTAGCGCCGTTGACGAATCTGTAGATGCCACCCGTTGTCAGGGTAAAGGCGG
CTGCCAGGGCGGCGATAAATGCCTGACCCACGCGCTGTGGCGTGATTTGAGCGACCGTCTCACC GGTTTTCTCA
ACAACATTACTT

93E3-6 (12X)

ycdR gene (complement)– orf, function unknown; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCCGCTTTAA
AAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAAGCCATTCGCGGTCCACATAT
TAAAACTGCACGAAATATTTTTGCACCTCCGGTAATACAACCTGAAAAGTGAAGCCTGGTTTGCACAGA
ATTATGCTGATTTCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCTGGAAGGTGTGCG
CAGAAAAATCGGCTGACCAATGGTTAATAACAATTGACCAATCAAATTA AAAACATCCCTCAGGCTAAA
GACAAATCTATTTTAGAATTACAGGC

96B10-1 (11X)

nhaR - regulator, transport of sm molecules - cations; encodes a positive regulator for nhaA(a Na/H antiporter)
stimulates transcription of osm-c

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000112

Protein Accession # AAC73131

NCAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACTTAATGATTTTTACAAAATCATTAGGGGATTCATCAG
GTTTATGCTGACTTAATTGCTCCAGCAGCATTTCGTGGGTGGATTCTGAAGCAGCGAAGATGAATGGGC
TCGCCTTCTACCACTGCGGCGTTAAGTACGCTACTGACCAGGCGTTTGGAAAGTGCATCAGCCACGCC
AACGTCAAACAATAAATTGGATTCTTTGCGATAGTTCACAATATCCNNC NNNNCCGTACTAGTCGACG
CGTGGCCAN

102G9-5 (5X)

leuO gene – Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAACNCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACAAAATCATTAGGGGATTCATCAG

AGTTAAGTGTGACAAAGTGGAGTTAAGTATGCCANAGGTACAAACAGATCATNCAGAGACGGNGGAGT
TAAGCAAACCACAGCTACAGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAGGA
NCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCNNNGCNGNNACTAGTTTCGACGCGTGG
CCNCATANNATGTNTCANNNTTCNNNNCTCTTCNNNTTGTCTCCCTTNNCCCTCTTCCNGCCCCCANNNC
GTCTNNTNTNATCANNNGNNCTTNNCNTACGACTN

106B2-6 (5X)

leuO gene – same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAACCCNTNGGATCCNG
CATCATATGACAAGANGTTGTATCCACCTTAACCTTAATGATTNTTACCAAANTCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGTGGAGTTAAGCAA
ACCACAGCTACNGCATGGTCGATCTCAACTTNTTAACCGTTNTCGATGCCGTGATGCAGGAGCAAAACATTACT
NCGTGCCGNTCATGTTCTGGGAATATCCCNNGGNNACGTNCTAGTCNANGCGTGGCCAANNNGNTNNGGNNCT
NANTCACAGNANCTTTANNNGTN

109B4-4 (2X)

Between two protein binding sites (complement) - 1)central position to predicted promoter: -0.5/LexA predicted site and 2)documented lrp site/ central position to leuABCD promoter:- 156.5

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AGCNCGCCGACNTCCCGGATCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTNTTACCAAATCATTAGGGGATTCATCAG
TCGGTAGTTAAGCAGAAATTAATATCGCTTACTTTAACCACCGCAGCACAATTAGCTAATTTTACGGAT
GCAGAACTCACGCTGGCGGGACGTTTTTATTGCGTCAGGGTTGACATCCGTTTTTGTATCCAGTAACTC
TAAAAGCATATCGCCCCCNCNGTACTAGTCGACGCGTGGCCANAACNCGNNNTCCANTNTNNCC

110G8-2 (9X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

GNAANGNAAAACNCGCCGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTNTTACCAAATCATTAGGGGATTCATCAG
NACNGCANNATTGNNCCACGGNGGANTAANTNGCCCCNGNTTGNNTTCTCGCTGNTAANGANAAATA
ACGTCTTTATAACGANCGCGAGTNAATAACGCGCCAAGATGATCAACCTGAATACNCTGGTACTGGGC
AGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCGATCGGCAA
TGGCATAACGNTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTTCGGCATGAATATCA
GNNNTTGTGNTAGNACNACGCGTGGNCAAAACAT

115C12-5 (16X)

ycdR gene (complement) – orf unknown function; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGCTTAATACCGGCATCCACGCATAGATGTTTACACCTGAGCGGGTACGTAATTGCCAGGCAACCCGA
CTAAAAATATCTGCTTTTCATTGGNCTNANACAANCNGGNGANCCAGACCTCTTTGACCAGCCCATCACC
ATCGGGATCAGCAAATGCCTGCAAATACACGGTTGATATTTGCATATCTTTCCCCNCGTACTAGTCGA
CGCGTGGCCACATTACTTNTANTNTANNANTGGATCCNANTNANNCGGNTNTANCTNGCCTTGNANGG
GNGNNANNATTATCENNCTGCCNNGACNAANT

123F5-6 (4X)

modA gene - transport, small molecules: anions; molybdate-binding periplasmic protein; permease

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73850

TTTNGAAACACGCCGNACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGGATTATGCGGTTGATAAAAAAGCGATCGATACAGCTACGCGTCAGACACTGCTCGGCAATAGCCTG
GTCGTTGTAGCACCAGAAAGCCAGCGTGCAGAAAGATTTACCATCGACAGCAAAACCAACTGGACTTC
ACTGCTGAATGGCGGTCGCTGGCGGTTGGCGATCCGGAACATGTTCCCGCTGGCATTATGCAAAAG
AAGCACTGCNAAAACCTGGGCGCATGGGATACNCTCNCTCCGAAAATGGNCCNCNTAAGNTGNTCCT
AGGGGNNCNCNCGCNGGTACACACNTAATCGAACC

125A7-1 (2.5X)

rbsK gene - enzyme, degradation of small molecules: carbon compounds; ribokinase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000452

Protein Accession # AAC76775

GCAAAAACGANNCGGCCAAG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GAAAGGGCAGCNTTANCGCCGGCATGAATACCGATGACATTCTACCTTCGCCATTAACAAAAATCAN
CGCCACACCTGTTGATTGCTCTTGTATCTCGCTGACCGGAGTAANATCCCCNTNNNGNACTAGTCNA
CGCGTGGCCATNAANTTCNNNCGACCNANTANGACCNANTCCTGNNNTTAANNCCNCGNNTNCCNTANTT
GCNCCANNN

125E4-1 (24X)

insB_4/insA_3/insA_2 genes (complement) - all three have the same probability score and identities,89% -
IS,phage,Tn; transposon-related function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

CACANCCGNACATCNGCGNT
ATNNCTACTNANAATGNCGTGAANTATTCNCTGACNTNACACTTACACCGNNTCTCATNCCGGTANGC
ACCACANAAANNNTGAATATGAGGCATGAATGGTNGTTGGANGCCGGGTAACAGCCNTCATTATGGG
NGTTGGCCTCAACACGATTTTCTCCNTTTAAAAAACTCACGCCGNTACCCTGTAACCTCGCACCATAC
TGGCAGGGCAGCNGACNGATTGCGCTGCGCATGAAATGNANAAACNNTGGGGATNACCAGGGNGTA
AATCTNGCCAGCGATNNCTGNNTTNTCTTNTGANANGATNCNGAAAANGGGGGNTGCNCNCGTNTN
CCGGNAAACATCNNTAATAAACTGGGGCCAAAGTAAACGTGCGGATATCCAATCCANNNGTACTA
NTCGACGCGTGGCCANNACTGNC

126C5-4 (7.5X)

leuO gene - same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

NNACGCTNCGGNNCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGTT
AAGCAAACACAGTCTACGCATGGTCGATCTCAACTATTAACCGTTTTTCGATGCCGTGATGCAGGAGC
AAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCCCCNCTNNGTACTAGTCGACGCGTGGCCA
NN

130E8-4 (24X)

Between yecK and cutC genes (complement) - in a protein binding area with no predicted promoter; TyrR predicted site

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

ATNCNCGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAN
NGTCCAGTAATTCAATTANAGGAATCTATGCGNGGGANAAACGGNTGGCNGCTNCNCGCTAANGCNA
ANAANTAANCCNCTNNNNCTANGTATNNNNGGGNCNNTNNNANNNCNGNTTTCT

130G11(2.5X)

aroD gene – enzyme: amino acid biosynthesis: chorismate; 3-dehydroquinase dehydratase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000264
Protein Accession # AAC74763

ANNCNCGACCGG
GNTCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TCNGGCCGANCNGGCNATTTCCACCGAGGCTTATNTCCNCCNNTNTCGNNCTAGNCGNNGCNTGGCCA
NGNTTNCGNCCNNTNACNCTCCATNANTNTNCCNCTNTCNCNNTACNGTGCCCGNGNATNC
CCNTCCTCCGTGCGCCCCCNNGCTTAGCNGCANNANTGGCCNNNNNNCAANTTANGACGATCNGCC
NGCCCNNTNAAACNGGTTNGCCATNTNCTNCTNTTATN

140B5-1 (9X)

miaA gene – enzyme, Aminoacyl tRNA synthetases, tRNA modification; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000489
Protein Accession # AAC77128

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGGCAAGTCCGTATGCAAATCTCCTCGGGCAAAAAGCGCCCGGACTTCTGCTTCAAAACCTGAAGCCA
ACATCTGATGAAAACGCTGCTCAATGCGTTGATGGAGCAGTTACGGCTCGCCGGGGCGATGGCGAAC
TGATGCACCTGATACGGTAGAGCGTCTCCTGACGTTTGCCTCAGTTCCGTTAAAGTTTTACCCGAAATG
AAAAAACTTCCAGTGCCCGGAAAGCCTTTGTGGATCATTTGGATGAATCCTTGCTGCCGCAACCGG
ATCTACCTCCTGAAGTTGACGATGCAATGACTCCCAACCTTGCTCTGCCGCTGTTGCTCAATTCTGGC
CCGTACTTCCGGGTCTGCCGACGGTAGCGGCGACAACCCTTCCAGCAATGCCTTGAAAT

141G2-2 (16X)

yjjQ gene - putative regulator, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000507
Protein Accession # AAC77321

GNCGGATCCGG
TATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGGGCATCAACCAGATAGCTTCATTGCTTAAGAAAAAGTAATAAACTATCANCGCCCAAAAAA
CAGTGCATGCGTCTGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGCGCAG
GGTGCAAGAGAAGCTTAACCTGCCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCGAATTAAG
AAGAGAAATGTCGCACTC

141G4-6 (18X)

ycdS gene (complement) - putative outer membrane protein; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

NNNAAAGCACGCCGGACATCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ACCCAATATTGCCCCAGGGCGGAATAATTTGCCCCGCTTTTTTAATCGCTGATAGTGAGAAATAACG
TCTTTATAACGATCGCGAGTTATAACGCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTG
CGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCGATCGGCAATGGC
ATAACGTTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGCATGAATATCANC
GAATAGTACTAGTCGAC

145F10 (3X)

ykgK gene (complement) - putative regulator; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000136
Protein Accession # AAC73397

NNNNGAAGCNCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACCACGCCCCAATATTGCTATTGTAATACCAATAATTTGCTAAGGCCCTCTGACTTTCTGGCCGCAAT
CAATACGACCTGTTTCCCTTTACCGCGGATAACCATTCATTATCACGGTTTATAAATTCAGATAAAGA
ATCCGTAAGTATGATAAACACGAAATCTTTTCTAATTTTCTCCAACGATAGATAAATTAATCTGTC
GATATCCCCCNNCNNNGTACTAGTCGACGCGTGGCCA

150E3-6 (20X)

ycdP gene (complement) - orf, hypothetical protein unknown function

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_415540

NACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCCAGAAGCCGACTTCAGTTCTATTTTTGCTGGCAGTGGCGAATGCCGTCGTGTTAATTGTCTGGGCGCTGT
ACAATAAGCTGCGTTTTCAAAAACAGCAGCATCATGCAGCCTACCAATATACGCCGCAAGAATATGCAGAGAG
CTTAGCAATACCTGATGAGCTCTATCAGCAACTACAAAAAGCCACAGGATGAGCGTACACTTCACCAGCCAG
GGGCAAATAAAAAATGGTTGTTTCAGAAAAAGCGCTAGTCCGGGCATAAACACCCAAAAACAAAGCCCGGTTTCG
CCGGGCTCTGCACCGATAACACACTTAACCTGTAGGCATGCAGCGTACGTTGGCAAAGTGCCGAACGTACGCAN
T

150G7-2 (4X)

prfC gene- Factor; protein translation and modification; peptide chain release factor RF-3.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000508

Protein Accession # AAC77328

ANACNCGTCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTANGGGATTTCATCAG
TGTGGTGTCCGGTAAATATGAAAAAGGCATNAACTGCNCCACGAGCCCACTGCNAANGATGNGGNA
ATCTCCGCCCGCNGCCTCTCTGGCNGGTNNCCGTTCTCACCTTNNACACCNCCCCNNGCTCNCNTNCN
CTCCCNACNNCNCNTTCTCTCNGCANCCCACTTATCTNCCNNCNCCTCCCNACGNNTCCCNCCCC
NCNGNNCNCANTGNNTTGGCTNNCGNCCNNNANNCNCNCTCCTGGCCTCNCNTTACNCNN

155F4-4 (20X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

NNCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
CACTTGTTGCCACGTGGCAAAATATTCTCGATCGACCAACTCATCGCCAAATTTTACTTGTTTATCCGG
TGGCATATCNCNNCCNNNCGTACTAGTCGACGCGTGGCCANN

160A8-6 (20X)

yjjQ gene - putative regulator; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000507

Protein Accession # AAC77321

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
GGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAACTATCAGCGCCCCAAAAAACAGTG
CGATGCGTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGCGCAGGGTGC
AAGAGAACTTAACCTGCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCGAATTAAGAAGAG
AAATGTCGCACTCATAGAAAAATGCGTCATGAGTAGTATCGGTATTGAGAGTTTATTCAGAAAGTTTG
CGGGTAACCCTTATAAGCTCCATACCTATACCAGTCAGGAGTCATTCAGGATGCCATGTCGCGGATA
TCCNCCNCCNCGTACTAGTCGACGCGTGGCCAA

169G4-6 (18X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

AAAANCNCGCCGGACATCCCGGATCCGGGATCAT
ATGACAAGGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
TATTAATCGCCAATAATCCCTCATTAAGAGTTTGCCAGCAAATTATTACCGTACAGGAAAAATCA
CCACAACGGATAATGCATATCNCNCCNNNNNGTACTAGTCGACGCGTGGCCACANAN